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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/672,515	09/25/2003	Peter Adorjan	5013.1022cip	1178

22504 7590 03/20/2006

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EXAMINER	
NEGIN, RUSSELL SCOTT	

ART UNIT	PAPER NUMBER
1631	

DATE MAILED: 03/20/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/672,515	ADORJAN ET AL.	
	Examiner	Art Unit	
	Russell S. Negin	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 December 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-97* is/are pending in the application.

4a) Of the above claim(s) *18-24,26-43,45-47 and 53-97* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-17,25,44 and 48-52* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election of Group I, Species A, C, H, and S in the reply filed on December 16, 2005 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claims 18-24, 26-43, 45-47, and 53-97 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected Group or Specie, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on December 16, 2005.

Claims 1-17, 25, 44, and 48-52 are under examination in this Office action.

Claim Objections

Claims 3-6 are objected to because of the following informalities:

Claims 3-6 invoke lists without introducing them with the appropriate "colon (:)" indicator. In claim 3, the phrase "at least one of cells, cellular components,..." needs to be modified. In claim 4, the phrase, "at least one of cell lines, biopsies, blood,..." needs correction. In claim 5, the phrase, "at least one of tissue from eyes, intestine, kidney,..." needs correction. In claims 6, the phrase "at least one of the phenotypic information and the phenotypic parameter of interest..." needs correction.

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-17, 25, 44, and 48-52 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-17, 25, 44, and 48-52 are rejected for having or being dependent from a claim with the term "disjunct." The metes and bounds for such a term is not clearly defined in the disclosure. Thus, the definition of the word disjunct phenotypes is ambiguous. For the purposes of examination, this term will mean distinct or different such that there is no overlap.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-4, 6-10, and 48 are rejected under 35 U.S.C. 102(b) as being anticipated by Janousek et al. [Molecular and General Genetics, vol. 250, pp. 483-490, 1996].

Claims 1-4, 6-10, and 48 state:

1. A method for selecting epigenetic features, comprising the steps of:

a) collecting and storing biological samples containing genomic DNA;
b) collecting and storing available phenotypic information about the biological samples so as to define a phenotypic data set;
c) defining at least one phenotypic parameter of interest;
d) dividing the biological samples into at least two disjunct phenotypic classes of interest using the defined phenotypic parameters of interest;
e) defining an initial set of epigenetic features of interest;
f) analysing the defined epigenetic features of interest of the biological samples so as to generate an epigenetic feature data set;
g) selecting relevant epigenetic features of interest and/or combinations of epigenetic features of interest of the defined epigenetic features of interest, the relevant epigenetic features of interest and/or combinations of epigenetic features of interest being relevant for epigenetically-based prediction of the at least two phenotypic classes of interest; and
h) defining a new set of epigenetic features of interest based on the relevant epigenetic features of interest and/or combinations of epigenetic features of interest generated in step g).

2. The method as recited in claim 1 further comprising repeating steps f) and g) based on the new set of epigenetic features of interest defined in step h).

3. The method as recited in claim 1 wherein the biological samples include at least one of cells, cellular components which contain DNA, sources of DNA, tissue embedded in paraffin and histologic object slides.

4. The method as recited in claim 3 wherein the sources of DNA include at least one of cell lines, biopsies, blood, sputum, stool, urine and cerebral-spinal fluid.

6. The method as recited in claim 1 wherein at least one of the phenotypic information and the phenotypic parameter of interest are selected from the group consisting of kind of tissue, drug resistance, toxicology, organ type, age, life style, disease history, signaling chains, protein synthesis, behavior, drug abuse, patient history, cellular parameters, treatment history and gene expression and combinations thereof.

7. The method as recited in claim 1 wherein the epigenetic features of interest include cytosine methylation sites in DNA.

8. The method as recited in claim 1 wherein the initial set of epigenetic features of interest is defined using preliminary knowledge data about their correlation with phenotypic parameters.

9. The method as recited in claim 1 wherein the relevant epigenetic feature or a combination of epigenetic features is relevant for epigenetically-based prediction of said phenotypic classes of interest when at least one of an accuracy and a significance of the epigenetically-based prediction of the phenotypic classes of interest is likely to

decrease by exclusion of the corresponding epigenetic feature data of the epigenetic feature data set.

10. The method as recited in claim 1 wherein step d) is performed so as to divide the biological samples in two disjunct phenotypic classes of interest.

48. The method as recited in claim 2 wherein the repeating steps f) and g) is performed until a defined number of the epigenetic features of interest and/or combinations of epigenetic features of interest are selected.

Janousek et al. investigate cytosine methylation sites in DNA as the epigenetic feature under consideration. The objective of this article is to show specifically how this epigenetic feature affects the DNA molecules in a dioecious plant to cause selection of the sexual phenotype. Thus, different means of selecting this epigenetic feature are likely to result in specific sexual differentiation. As the last sentence of the abstract states on page 483, "The data presented indicate that female sex suppression in *M. album* XY males is dependent on methylation of specific DNA sequences and can be heritably modified by hypomethylating drugs."

In Janousek et al, on page 484, second column, under "DNA methylation analysis," it is stated, "total DNA was isolated from fresh leaves according to a standard protocol..." It is inherent in this statement that this isolation means that the DNA was collected and stored for future use in the study.

In Janousek et al., on page 485, column 1 in Table 1, this table show the data collection and storage of available phenotypic information about said biological samples, selection of at least one phenotype based on the available phenotypic information, and division of the phenotypes into classes. It was necessary to determine the sexual phenotypic information of each of the plants to construct Table 1. The

phenotype selected was the sexual phenotype. The plants were then divides into classes (one class for each sex) based on the sex of each of the plants.

The epigenetic features of interest include cytosine methylations. As stated in Janousek on page 843, column 2, second sentence of the introduction, "A large body of literature indicates that these processes are often correlated with cytosine methylation in corresponding DNA sequences." The method of measurement of this feature is complex and described on page 484, column 2, the last three paragraphs.

Janousek shows that the epigenetic feature of cytosine methylation is responsible for the phenotypic differentiation, as stated on page 484, line 45-48, column 1, "suppression of female differentiation in *M. album* males can be inhibited with the hypomethylating drug 5-azaC." Thus, hypomethylation of cytosines results in inhibition of suppression of female differentiation. The prediction of said phenotypic classes of interest occurs in the previous paragraph (page 484, column 1, lines 28-32), with a hypothesis which states, "The Y chromosome of *M. album.* harbors both male-determining and gynoecium-suppressing genes. Products of these suppressor genes inactivate female-determining genes (putatively located on the X and/or outosomes), so that XY plants develop stamens only."

Janousek also teaches how to define a set of epigenetic features of interest based on the relevant epigenetic features of interest previously described. This is taught in the abstract, page 483, column 1, lines 14-18 which state, "Southern hybridization analysis with a repetitive DNA probe showed that the 5-azacytidine-treated plants were significantly hypomethylated in CG doublets, but only to a minor degree in

CNG triplets." Thus, the general, initial epigenetic feature of cytosine methylation is narrowed to a new set of epigenetic features, namely hypomethylation of CG base pairs.

This method is repeated several times as shown in Janousek, Figures 3 and 4. The cellular components in the plant cell lines contain DNA. The sexual phenotype of the cell is considered, which is a type of gene expression and cellular parameter. With a decrease in the number of samples provided and the amount of cytosine methylation that occurs, epigenetically-based prediction of phenotypic classes of interest is likely to decrease. The separate, disjunct classes of phenotypes are the sexes of the individual plants.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to

consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 2, 10-16, 25, 44, and 52 are rejected under 35 U.S.C. 103(a) as being unpatentable over Janousek et al. [Molecular and General Genetics, vol. 250, pp. 483-490, 1996] in view of Cutis et al. [Annals of Human Genetics, volume 65, pages 95-107, January, 2001].

Claims 1, 2, 10-16, 25, 44, 49-50, and 52 state:

1. A method for selecting epigenetic features, comprising the steps of: a) collecting and storing biological samples containing genomic DNA; b) collecting and storing available phenotypic information about the biological samples so as to define a phenotypic data set; c) defining at least one phenotypic parameter of interest; d) dividing the biological samples into at least two disjunct phenotypic classes of interest using the defined phenotypic parameters of interest; e) defining an initial set of epigenetic features of interest; f) analysing the defined epigenetic features of interest of the biological samples so as to generate an epigenetic feature data set; g) selecting relevant epigenetic features of interest and/or combinations of epigenetic features of interest of the defined epigenetic features of interest, the relevant epigenetic features of interest and/or combinations of epigenetic features of interest being relevant for epigenetically-based prediction of the at least two phenotypic classes of interest; and h) defining a new set of epigenetic features of interest based on the relevant epigenetic features of interest and/or combinations of epigenetic features of interest generated in step g).

2. The method as recited in claim 1 further comprising repeating steps f) and g) based on the new set of epigenetic features of interest defined in step h).

10. The method as recited in claim 1 wherein step d) is performed so as to divide the biological samples in two disjunct phenotypic classes of interest.

11. The method as recited in claim 10 further comprising performing the epigenetically-based prediction of the at least two phenotypic classes of interest using a machine learning classifier.

12. The method as recited in claim 1 further comprising: selecting pairs of classes or pairs of unions of classes from the disjunct phenotypic classes of interest; and performing epigenetically-based prediction of each pair of classes or pair of unions of classes using a machine learning classifier.

13. The method as recited in claim 11 wherein the selecting of step g) includes: defining a candidate set of and/or combinations of epigenetic features of interest of the defined epigenetic features of interest; defining a feature selection criterion; ranking the candidate set of epigenetic features of interest and/or combinations of epigenetic features of interest according to the feature selection criterion; and selecting the highest ranking epigenetic features of interest and/or combinations of epigenetic features of interest.

14. The method as recited in claim 13 wherein the candidate set of epigenetic features of interest is the set of all subsets of the defined epigenetic features of interest.

15. The method as recited in claim 13 wherein the candidate set of epigenetic features of interest is a set of all subsets of a given cardinality of the defined epigenetic features of interest.

16. The method as recited in claim 13 wherein the candidate set of epigenetic features of interest is a set of all subsets of cardinality 1 of the defined epigenetic features of interest.

25. The method as recited in claim 13 wherein the feature selection criterion includes a training error of the machine learning classifier trained on respective epigenetic feature data of the epigenetic feature data set corresponding to the candidate set of epigenetic features of interest and/or combinations of epigenetic features of interest.

52. The method as recited in claim 1 further comprising training a machine learning classifier using a feature data set corresponding to the defined new set of epigenetic features of interest.

Janousek et al. teach the method of identifying epigenetic features to deduce phenotypic properties. However, they do not teach how to rank results or use machine learning classifiers to figure these accurate phenotypes.

Curtis et al., entitled, "Use of an artificial neural network to detect association between a disease and multiple marker genotypes," use artificial neural networks to classify between disease and multiple marker genotypes. Without giving a precise definition of machine learning classifier in the specification, a neural network is an example of such a machine learning classifier. The results in Curtis et al. are ranked

according to linkage to an inflicted mutation over the course of many generations (Table 4 on page 104). A cardinality of 1 (or equivalently 100%) is assigned to the most reported continuation and strength of the epigenetic feature (Table 4). There is network design and training associated with the neural network, as described in the second column of page 100 in Curtis.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to practice the empirical epigenetic/phenotypic method of Jarousek et al in view of the computational procedure of Curtis et al. because while both provide linkage of epigenetic to phenotypic features, Curtis et al. has the advantage of being applicable to more detailed quantification of epigenetic phenomena, including ranking of genotypes.

Claims 1, 10, 11, 13, and 17 are rejected under 35 U.S.C. 103(a) as being unpatentable over Jarousek et al in view of Curtis et al as applied to claims 1, 2, 10-16, 25, 44, and 52 above, and further in view of Spotorno et al [Evolucion Biologica, 1990, volume 4, pages 37-62].

Claims 1, 10, 11, 13, and 17 state:

1. A method for selecting epigenetic features, comprising the steps of: a) collecting and storing biological samples containing genomic DNA; b) collecting and storing available phenotypic information about the biological samples so as to define a phenotypic data set; c) defining at least one phenotypic parameter of interest; d) dividing the biological samples into at least two disjunct phenotypic classes of interest using the defined phenotypic parameters of interest; e) defining an initial set of epigenetic features of interest; f) analysing the defined epigenetic features of interest of the biological samples so as to generate an epigenetic feature data set; g) selecting relevant epigenetic features of interest and/or combinations of epigenetic features of interest of the defined epigenetic features of interest, the relevant epigenetic features of interest and/or combinations of epigenetic features of interest being relevant for epigenetically-based prediction of the at least two phenotypic classes of interest; and h) defining a new set of

epigenetic features of interest based on the relevant epigenetic features of interest and/or combinations of epigenetic features of interest generated in step g).

10. The method as recited in claim 1 wherein step d) is performed so as to divide the biological samples in two disjunct phenotypic classes of interest.

11. The method as recited in claim 10 further comprising performing the epigenetically-based prediction of the at least two phenotypic classes of interest using a machine learning classifier.

13. The method as recited in claim 11 wherein the selecting of step g) includes: defining a candidate set of and/or combinations of epigenetic features of interest of the defined epigenetic features of interest; defining a feature selection criterion; ranking the candidate set of epigenetic features of interest and/or combinations of epigenetic features of interest according to the feature selection criterion; and selecting the highest ranking epigenetic features of interest and/or combinations of epigenetic features of interest.

17. The method as recited in claim 13 wherein the defining the candidate set of epigenetic features of interest and/or combinations of epigenetic features of interest is performed by subjecting the epigenetic feature data set to principal component analysis, principal components of the principal component analysis defining the candidate set of epigenetic features of interest and/or combinations of epigenetic features of interest.

Jarousek et al and Curtis et al. teach the method of the claims 1, 10, 11, and 13-specifically finding a linkage between epigenetic and phenotypic characteristics with and without a machine learning classifier.

Jarousek and Curtis, however, do not teach the feature of a principal component analysis.

Spotorno, however, in their abstract, page 37, line 17-26 state, "Principal component analysis of 14 craniomandibular and four external body measurements of 17 species distribute specimens... The distal bacular absence, modified accessory glands, increased body size and young with exceptional morphometric scores found in *Abrothrix longipilis* may compose an epigenetic cascade of developmental bounded phenotypes

probably induced by a neonatal testosterone delay." Thus, principal component analysis is used by Spotorno to identify the linkage between epigenetic and phenotypic parameters.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to practice Jarousek et al in view of Curtis et al as applied to claims 1, 2, 10-16, 25, 44, and 52 above, and further in view of Spotorno et al because Sportorno teaches an alternative theoretical and mathematical means of approaching the same problem and shows the same linkage between epigenetic and phenotypic parameters.

Double Patenting

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422

F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Regarding use of the specification in obviousness-type double patenting rejections, the MPEP states in section 804:

When considering whether the invention defined in a claim of an application is an obvious variation of the invention defined in the claim of a patent, the disclosure of the patent may not be used as prior art. This does not mean that one is precluded from all use of the patent disclosure.

The specification can always be used as a dictionary to learn the meaning of a term in the patent claim. In re Boylan, 392 F.2d 1017, 157 USPQ 370 (CCPA 1968). Further, those portions of the specification which provide support for the patent claims may also be examined and considered when addressing the issue of whether a claim in the application defines an obvious variation of an invention claimed in the patent. In re Vogel, 422 F.2d 438, 441-42, 164 USPQ 619, 622 (CCPA 1970). The court in Vogel recognized "that it is most difficult, if not meaningless, to try to say what is or is not an obvious variation of a claim," but that one can judge whether or not the invention claimed in an application is an obvious variation of an embodiment disclosed in the patent which provides support for the patent claim. According to the court, one must first "determine how much of the patent disclosure pertains to the

invention claimed in the patent" because only "[t]his portion of the specification supports the patent claims and may be considered." The court pointed out that "this use of the disclosure is not in contravention of the cases forbidding its use as prior art, nor is it applying the patent as a reference under 35 U.S.C. 103, since only the disclosure of the invention claimed in the patent may be examined."

Claims 1-2, 6-7, 11-17, 44, and 48-50 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-2, 4-5, 9-15, 38, 42-44, respectively, of copending Application No. 10/106,269. Although the conflicting claims are not identical, they are not patentably distinct from each other because the current application limits the classes of phenotypes to disjunct classes while Application No. 10/106,269 does not. However, in paragraph [0021] of the specification of copending application 10/106,269, applicants state, "In one particularly preferred embodiment, the phenotypic parameters of interest are used to divide the biological samples in two disjunct phenotypic classes of interest." Thus, disjunct, phenotypic parameters are present in both applications.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Ardin Marschel, Ph.D., Supervisory Patent Examiner, can be reached at (571) 272-0718.

Any inquiry of a general nature or relating to the status of this application should be directed to Legal Instrument Examiner, Tina Plunkett, whose telephone number is (571) 272-0549.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

RSN 3/14/06

3/14/06

15 March 2006

JOHN S. BRUSCA, PH.D
PRIMARY EXAMINER